

Query= SEQ ID NO:8
 (924 letters)

Sequences producing significant alignments:

	Score (bits)	E Value
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AC091612.4.1.180657	<u>1824</u>	0.0
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>AC091612.4.1.180657
 Length = 180657

Score = 1824 bits (920), Expect = 0.0
 Identities = 923/924 (99%)
 Strand = Plus / Minus

Query: 1	atgaatcacagcgttgtaactgagttcattattctgggcctcaccaaaaagcctgaactc	60
Sbjct: 155813	atgaatcacagcgttgtaactgagttcattattctgggcctcaccaaaaagcctgaactc	155754

Query: 61	caggggaattatcttccctcttttttctcattgtctatcttggtggttttctcggaacatg	120
Sbjct: 155753	caggggaattatcttccctcttttttctcattgtctatcttggtggttttctcggaacatg	155694

Query: 121	ctcatcatcattgccaaaatctatagcaacaccttgcatacgcccagtgatgttttcctt	180
Sbjct: 155693	ctcatcatcattgccaaaatctataacaacaccttgcatacgcccagtgatgttttcctt	155634

Query: 181	ctgacactggctgttggtggacatcatctgcacaacaagcatcataccgaagatgctgggg	240
Sbjct: 155633	ctgacactggctgttggtggacatcatctgcacaacaagcatcataccgaagatgctgggg	155574

Query: 241	accatgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttg	300
Sbjct: 155573	accatgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttg	155514

Query: 301	ttcacatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctat	360
Sbjct: 155513	ttcacatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctat	155454

Query: 361	gtggccatttggttccctcttcattacagtactattatgaaccaccatattgtgtgtagcc	420
Sbjct: 155453	gtggccatttggttccctcttcattacagtactattatgaaccaccatattgtgtgtagcc	155394

Query: 421	ttgctcagcatggtcatggctattgcagtcaccaattcctgggtgcacacagctcttatc	480
Sbjct: 155393	ttgctcagcatggtcatggctattgcagtcaccaattcctgggtgcacacagctcttatc	155334

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Query: 481 atgaggttgactttctgtggggccaaacaccattgaccacttcttctgtgagataacccca 540
|||||
Sbjct: 155333 atgaggttgactttctgtggggccaaacaccattgaccacttcttctgtgagataacccca 155274

Query: 541 ttgctggctttgtcctgtagccctgtaagaatcaatgaggtgatgggtgatgttgctgat 600
|||||
Sbjct: 155273 ttgctggctttgtcctgtagccctgtaagaatcaatgaggtgatgggtgatgttgctgat 155214

Query: 601 attaccctggccataggggactttattcttacctgcatctcctatgggtttatcattgtt 660
|||||
Sbjct: 155213 attaccctggccataggggactttattcttacctgcatctcctatgggtttatcattgtt 155154

Query: 661 gctattctccgtatccgcacagtagaaggcaagaggaaggccttctcaacatgctcatct 720
|||||
Sbjct: 155153 gctattctccgtatccgcacagtagaaggcaagaggaaggccttctcaacatgctcatct 155094

Query: 721 catctcacagtgggtgaccctttactattctcctgtaatctacacctatatccgccctgct 780
|||||
Sbjct: 155093 catctcacagtgggtgaccctttactattctcctgtaatctacacctatatccgccctgct 155034

Query: 781 tccagctatacatttgaaagagacaagggtggtagctgcactctatactcttgtagactccc 840
|||||
Sbjct: 155033 tccagctatacatttgaaagagacaagggtggtagctgcactctatactcttgtagactccc 154974

Query: 841 acattaaacccgatgggtgtacagcttcagaatagggagatgcaggcaggaattaggaag 900
|||||
Sbjct: 154973 acattaaacccgatgggtgtacagcttcagaatagggagatgcaggcaggaattaggaag 154914

Query: 901 gtgtttgcatttctgaaacactag 924
|||||
Sbjct: 154913 gtgtttgcatttctgaaacactag 154890

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Taxonomy

OMIM

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☐ 1: AC091612. Homo sapiens chro...[gi:18497169]

Links

LOCUS AC091612 180657 bp DNA linear HTG 05-FEB-2002
 DEFINITION Homo sapiens chromosome 1 clone RP11-656022, WORKING DRAFT

SEQUENCE, 1 unordered piece.

ACCESSION AC091612 AL390860

VERSION AC091612.4 GI:18497169

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 180657)

AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 180657)

AUTHORS Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J., Ivey,R.G. and
 Haugen,E.D.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-2001) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

COMMENT On Feb 5, 2002 this sequence version replaced gi:15487406.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchtgs@u.washington.edu

Drafting Center: SC

----- Project Information

Center project name: chr-1

Center clone name: RP11-656022 (sc0182)

----- Summary Statistics

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 180536 bases at least Q40

Consensus quality: 180650 bases at least Q30

Consensus quality: 180657 bases at least Q20

Insert size: 194815; 11.0% error; agarose-fp

Insert size: 180657; sum-of-contigs

Quality coverage: 8.4x in Q20 bases; agarose-fp

Quality coverage: 9.0x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.

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